

IN THE SPECIFICATION:

Please amend paragraph [0030] as follows:

--[0030] In one embodiment, an isolated polypeptide comprising the amino acid sequence Y (Trp/Phe) Xaa₁ Xaa₂ Xaa₃ Xaa₄ Xaa₅ (Trp/Phe) Xaa₆ Xaa₇ (Trp/Phe) Z (SEQ ID NOs: 17-20) is provided. Y, which may or may not be present, is a peptidic structure containing at least one cysteine residue and having the formula (Xaa)_n. Xaa is any amino acid residue and n is an integer from 1 to 20. Z, which may or may not be present, is a peptidic structure containing at least one cysteine residue and having the formula (Xaa)_n, wherein Xaa is any amino acid residue and n is an integer from 1 to 20. The amino acid residues of in Xaa₁ through Xaa₇ can be any amino acid and the amino acid residues of Xaa₁ through Xaa₅ are positively charged. --

Please amend paragraph [0031] as follows:

--[0031] In another embodiment, an isolated polypeptide comprising the amino acid sequence Y (Trp/Phe) Xaa₁ Xaa₂ Xaa₃ Xaa₄ Xaa₅ (Trp/Phe) Xaa₆ Xaa₇ Xaa₈(Trp/Phe) Z (SEQ ID NOs: 21-24) is provided. Y, which may or may not be present, is a peptidic structure containing at least one cysteine residue and having the formula (Xaa)_n. Xaa is any amino acid residue and n is an integer from 1 to 20. Z, which may or may not be present, is a peptidic structure containing at least one cysteine residue and having the formula (Xaa)_n, wherein Xaa is any amino acid residue and n is an integer from 1 to 20. The amino acid residues of Xaa₁ through Xaa₈ is any amino acid, and at least two of the amino acid residues of Xaa₁ through Xaa₅ are positively charged. --

Please amend paragraph [0059] as follows:

--[0059] To verify that the DWGKGGRWRLWPGASGKTEA (SEQ ID NO:2) peptide would identify Aβ₁₋₄₀ amyloid independently of its presence in bacteriophage, this peptide was produced in recombinant form as a fusion protein with thioredoxin. Cysteines were engineered at either end of the peptide in the fusion construct, along with several other residues from the phage coat protein. The ultimate or penultimate residue was engineered to be a proline to mimic predicted beta turn at either side of